WE CLAIM:

1. An oligomer comprising a base sequence of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:42, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52 or SEQ ID NO:57.

2. An oligomer of Claim 1, wherein the base sequence is that of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:17, SEQ ID NO:18 or SEQ ID NO:45.

3. An oligomer of Claim 1, further comprising a backbone that includes at least one 2'-methoxy RNA group, at least one 2' fluoro-substituted RNA group, at least one peptide nucleic acid linkage, at least one phosphorothioate linkage, at least one methylphosphonate linkage or any combination thereof.

4. An oligomer of Claim 3, wherein the base sequence comprises the sequence of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20 or SEQ ID NO:45, and the backbone comprises at least one 2'-methoxy RNA group.

5. An oligomer consisting of a base sequence of SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:16, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:54, SEQ ID NO:55 or SEQ ID NO:56.

6. The oligomer of Claim 5, wherein the base sequence is SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13 or SEQ ID NO:16.

7. An oligomer of Claim 5, wherein the base sequence is joined by a backbone that includes at least one 2'-methoxy RNA group, at least one 2' fluoro-substituted RNA group, at least one peptide nucleic acid linkage, at least one phosphorothioate linkage, at least one methylphosphonate linkage or any combination thereof.

8. A labeled oligomer comprising:

a base sequence of SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55 or SEQ ID NO:56; and

a detectable label joined directly or indirectly to the base sequence.

9. The labeled oligomer of Claim 8, wherein the detectable label is a luminescent compound.

10. The labeled oligomer of Claim 8, wherein the base sequence is joined by a backbone comprising at least one 2'-methoxy RNA group.

11. The labeled oligomer of Claim 10, wherein the base sequence is SEQ ID NO:16, SEQ ID NO:17 or SEQ ID NO:18, and the label is a chemiluminescent compound.

12. The labeled oligomer of Claim 11, wherein the base sequence is SEQ ID NO:16 containing an inosine at residue 7, and the label is an acridinium ester compound.

13. A method of detecting HIV-1 RNA in a biological sample, comprising the steps of:

providing a biological sample containing HIV-1 RNA;

contacting the biological sample with at least one capture oligomer comprising a base sequence that hybridizes specifically to a target region in LTR or *pol* sequences of HIV-1 RNA, thus forming a capture oligomer:HIV-1 RNA complex;

separating the capture oligomer:HIV-1 RNA complex from the biological sample;

then amplifying the LTR or *pol* sequences, or a cDNA made therefrom, using a nucleic acid polymerase *in vitro* to produce an amplified product; and

detecting the amplified product using a labeled detection probe that hybridizes specifically with the amplified product.

14. The method of Claim 13, wherein the contacting step uses a capture oligomer further comprising a tail sequence that binds to a complementary sequence immobilized on a solid support.

15. The method of Claim 13, wherein the base sequence of the capture oligomer that hybridizes specifically to a target region in LTR or *pol* sequences comprises a sequence of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:19 or SEQ ID NO:57.

16. The method of Claim 13, wherein the capture oligomer comprises the base sequence of at least one of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:20 or SEQ ID NO:45, or is any combination of oligomers of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:20 or SEQ ID NO:45.

17. The method of Claim 16, wherein the capture oligomer is any combination of at least two oligomers having base sequences selected from the group of SEQ ID NO:2, SEQ ID NO:4 and SEQ ID NO:6.

18. The method of Claim 16, wherein the capture oligomer is a combination of oligomers having base sequences of SEQ ID NO:20 and SEQ ID NO:6, or SEQ ID NO:45 and SEQ ID NO:6.

19. The method of Claim 13, wherein the amplifying step uses at least two amplification oligomers that bind specifically to LTR or *pol* sequences or complementary sequences thereof.

20. The method of Claim 19, wherein the amplifying step uses at least two amplification oligomers for amplifying LTR sequences selected from the group consisting of: SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37 and SEQ ID NO:38.

21. The method of Claim 19, wherein the amplifying step uses at least two amplification oligomers for amplifying *pol* sequences selected from the group consisting of:
SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:42, SEQ ID NO:43 and SEQ ID NO:44.

22. The method of Claim 13, wherein the amplifying step comprises a transcription-associated amplification method that includes:

at least one promoter-primer comprising a promoter sequence that is recognized by an RNA polymerase when the promoter sequence is double stranded, wherein the promoter sequence is covalently attached to the 5' end of

a LTR-specific sequence selected from the group consisting of SEQ ID NO:7, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31 and SEQ ID NO:33, or

a *pol*-specific sequence selected from the group consisting of SEQ ID NO:12 and SEQ ID NO:14; and

at least one primer comprising

a LTR-specific sequence selected from the group consisting of SEQ ID NO:9, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37 and SEQ ID NO:38, or

a *pol*-specific sequence selected from the group consisting of SEQ ID NO:10, SEQ ID NO:11 and SEQ ID NO:42,

provided that at least one LTR-specific promoter-primer is combined with at least one LTR-specific primer for amplifying a LTR target region, or at least one *pol*-specific promoter-primer is combined with

at least one *pol*-specific primer for amplifying a *pol* target region.

23. The method of Claim 13, wherein the amplifying step comprises a transcription-associated amplification method that includes:

at least one promoter-primer having:

a LTR-specific sequence selected from the group consisting of SEQ ID NO:8, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32 and SEQ ID NO:34, or

a *pol*-specific sequence selected from the group consisting of SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:43 and SEQ ID NO:44; and

at least one primer having

a LTR-specific sequence selected from the group consisting of SEQ ID NO:9, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37 and SEQ ID NO:38, or

a *pol*-specific sequence selected from the group consisting of SEQ ID NO:10, SEQ ID NO:11 and SEQ ID NO:42,

provided that at least one LTR-specific promoter-primer is combined with at least one LTR-specific primer for amplifying a LTR target region, or at least one *pol*-specific promoter-primer is combined with at least one *pol*-specific primer for amplifying a *pol* target region.

24. The method of Claim 23, wherein the amplifying step uses any of the following combinations of promoter-primers and primers:

promoter-primers of SEQ ID NO:13 and SEQ ID NO:15, with primers of SEQ ID NO:10 and SEQ ID NO:11;

promoter-primers of SEQ ID NO:13 and SEQ ID NO:15, with primers of SEQ ID NO:42 and SEQ ID NO:11;

promoter-primers of SEQ ID NO:43 and SEQ ID NO:15, with primers of SEQ ID NO:10 and SEQ ID NO:11;

promoter-primers of SEQ ID NO:13 and SEQ ID NO:44, with primers of SEQ ID NO:10 and SEQ ID NO:11;

promoter-primers of SEQ ID NO:7, SEQ ID NO:13 and SEQ ID NO:15, with primers of SEQ ID NO:9, SEQ ID NO:10 and SEQ ID NO:11;

a promoter-primer of SEQ ID NO:8, and a primer of SEQ ID NO:9;

a promoter-primer of SEQ ID NO:8, and a primer of SEQ ID NO:35;

a promoter-primer of SEQ ID NO:8, and a primer of SEQ ID NO:36;

a promoter-primer of SEQ ID NO:30, and a primer of SEQ ID NO:9;

a promoter-primer of SEQ ID NO:30, and a primer of SEQ ID NO:36;

a promoter-primer of SEQ ID NO:32, and a primer of SEQ ID NO:9;

a promoter-primer of SEQ ID NO:34, and a primer of SEQ ID NO:36;

a promoter-primer of SEQ ID NO:13, and a primer of SEQ ID NO:10; or

a promoter-primer of SEQ ID NO:7, and a primer of SEQ ID NO:9.

25. The method of Claim 13, wherein the detecting step uses at least one labeled detection probe having a base sequence selected from:

the LTR-specific group consisting of SEQ ID NO:16, SEQ ID NO:39, SEQ ID NO:40 and SEQ ID NO:41, or

the *pol*-specific group consisting of SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55 and SEQ ID NO:56, or

a combination thereof.

26. The method of Claim 13, wherein the detecting step uses a combination of at least two labeled detection probes having the base sequences of SEQ ID NO:16, SEQ ID NO:17 or SEQ ID NO:18.

27. The method of Claim 26, wherein the labeled detection probe of SEQ ID NO:16 has an inosine at position 7.

28. The method of Claim 13, wherein the detecting step uses at least one labeled detection probe having a base sequence selected from the LTR-specific group consisting of SEQ ID NO:16, SEQ ID NO:39, SEQ ID NO:40 and SEQ ID NO:41.

29. The method of Claim 13, wherein the detecting step uses at least one labeled detection probe having a base sequence selected from the *pol*-specific group consisting of SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55 and SEQ ID NO:56.

30. The method of Claim 13, wherein the detecting step uses at least one labeled detection probe that includes at least one 2'-methoxy backbone linkage.

31. The method of Claim 13, wherein:

the contacting step uses capture oligomers having the sequences of SEQ ID NO:2,

SEQ ID NO:4 and SEQ ID NO:6;

the amplifying step uses promoter-primers having the sequences of SEQ ID NO:8, SEQ ID NO:13 and SEQ ID NO:15 and primers having the sequences of SEQ ID NO:9, SEQ ID NO:10 and SEQ ID NO:11; and

the detecting step uses labeled detection probes having the sequences of SEQ ID NO:16, SEQ ID NO:17 and SEQ ID NO:18.

32. The method of Claim 13, wherein:

the contacting step uses at least two capture oligomers that hybridize to different sequences in the target region;

the amplifying step uses at least two different promoter-primers that hybridize to a first set of sequences within the target region and at least two different primers that hybridize to a second set of sequences within the target region; and

the detecting step uses at least two labeled probes that bind specifically to different sequences located between the first set and second set of sequences within the target region.

33. The method of Claim 32, wherein

the contacting step uses capture oligomers having the sequences of SEQ ID NO:4 and SEQ ID NO:6;

the amplifying step uses promoter-primers having the sequences of SEQ ID NO:13 and SEQ ID NO:15 and primers having the sequences of SEQ ID NO:10 and SEQ ID NO:11; and

the detecting step uses labeled probes having the sequences of SEQ ID NO:17 and SEQ ID NO:18.

34. The method of Claim 32, wherein the amplifying step uses at least two promoter-primers that hybridize to a first set of overlapping sequences within the target region, at least two primers that hybridize to a second set of overlapping sequences within the target region, or a combination thereof.

35. A kit comprising a plurality of oligomers having the sequences of SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17 and SEQ ID NO:18, wherein the oligomers having the sequences of SEQ ID NO:17 and SEQ ID NO:18 are labeled with a detectable label.

36. The kit of Claim 35, further comprising oligomers having the sequences of SEQ ID NO:8, SEQ ID NO:9 and SEQ ID NO:16, wherein the oligomer having the sequence of SEQ ID NO:16 is labeled with a detectable label.